GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: January 3, 2002, 20:10:34 ; Search time 271.41 Seconds
(without alignments)
16052.934 Million cell updates/sec

Title: US-09-497-822A-18
Perfect score: 5082
Sequence: 1 gagctctggacaaaattgag.....acaagcaaacaaaaaaaaaa 5082

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3595.8	70.8	3715	20	AAZ23424	Human androgen rec
2	3594.2	70.7	3715	12	AAQ12001	Full-length human
3	3547	69.8	3569	18	AAT63407	Androgen receptor
4	3545.4	69.8	3569	10	AAN91772	Human androgen rec
5	2486.4	48.9	4180	10	AAN91773	Rat androgen recep
6	2189.2	43.1	3217	12	AAQ12002	Full-length rat an
7	2185.8	43.0	3217	10	AAN91578	Rat androgen recep
8	1715.6	33.8	1810	22	AAF84342	Human androgen rec
9	711.8	14.0	1893	12	AAQ12008	TrpE/androgen rece
10	703.6	13.8	1731	12	AAQ12007	TrpE/N-terminal do
11	611.6	12.0	612	21	AAC70311	Single nucleotide
12	611.6	12.0	612	21	AAC70335	Single nucleotide
13	575.6	11.3	598	21	AAC70305	Single nucleotide
14	575.6	11.3	598	21	AAC70308	Single nucleotide
15	401.6	7.9	6244	16	AAQ76269	PhCMV*-1-controlle
16	401.6	7.9	6244	20	AAX81724	cDNA encoding rabb
17	401.6	7.9	6244	20	AAX27905	Rabbit progesteron
18	401.6	7.9	6244	20	AAX01369	PhCMV*-1 rabbit pr
19	401.6	7.9	6244	22	AAD09837	Rabbit progesteron
20	400	7.9	6244	16	AAT06872	PhCMV*-1 promoter
21	384	7.6	1231	14	AAQ37761	Sequence of a 1.23
22	384	7.6	3014	18	AAT94756	Human progesterone
23	384	7.6	3014	18	AAT84747	Human progesterone
24	383	7.5	2970	21	AAA53851	Sequence encoding
25	340.6	6.7	1329	12	AAQ12009	TrpE/AR androgen-b
26	320.8	6.3	358	21	AAC08780	Human secreted pro
27	310.8	6.1	7257	18	AAT68656	Green fluorescent
28	304	6.0	5775	9	AAN80920	Sequence encoding
29	298.6	5.9	5040	9	AAN80916	Sequence encoding
30	295.4	5.8	2334	18	AAV05701	Mutant nuclear glu
31	290.6	5.7	380	21	AAC70326	Single nucleotide
c 32	287.6	5.7	326	19	AAV17743	Human breast cance
33	262.2	5.2	1496	22	AAD06047	C7PBDVP16 construc
34	260.8	5.1	1404	22	AAD06061	VP16C7PR construct
c 35	234	4.6	234	15	AAQ72991	Androgen receptor
c 36	234	4.6	234	19	AAV17742	Human breast cance
37	203.4	4.0	855	21	AAC61421	DNA encoding a rat
38	201.8	4.0	855	19	AAT86659	Glucocorticoid rec
39	201.8	4.0	855	19	AAV02769	Rat glucocorticoid
40	201.8	4.0	855	21	AAZ57063	Rat glucocorticoid
41	201.8	4.0	855	21	AAZ92155	Glucocorticoid rec
42	195.6	3.8	2004	18	AAV05702	Chimeric Cre-LDB-G
43	195.6	3.8	6094	18	AAV05703	Plasmid pCre-LBD[G
44	194.6	3.8	239	21	AAC70338	Single nucleotide
45	194	3.8	1884	17	AAT31320	Glucocorticoid rec

ALIGNMENTS

RESULT 1
AAZ23424
ID AAZ23424 standard; DNA; 3715 BP.
XX
AC AAZ23424;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human androgen receptor DNA.
XX
KW Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;
KW huntingtin polypeptide; Machado-Joseph disease; SCA1; SCA2; SCA6;
KW atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;
KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;
KW dentatorubropallidoluysian atrophy; cell proliferation; cell survival;
KW neoplastic; malignant; autoimmune; fibrotic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 532..3288
FT /*tag= a
FT /product= "androgen receptor"
XX
PN WO9945944-A1.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US05250.
XX
PR 12-MAR-1998; 98US-0041886.
XX
PA (BURN-) BURNHAM INST.
XX

PI Bredesen DE, Rabizadeh S;
XX
DR WPI; 1999-561617/47.
DR P-PSDB; AAY33491.
XX
PT New proapoptotic dependence peptides, used to develop products for
PT treating, e.g. Alzheimer's disease -
XX
PS Disclosure; Page 86-90; 199pp; English.
XX
CC This invention describes novel pure proapoptotic dependence peptides
CC which comprise a sequence of an active dependence domain selected from
CC dependence polypeptides consisting of p75NTR, androgen receptor, DCC,
CC huntingtin polypeptide, Machado-Joseph disease gene product, SCA1, SCA2,
CC SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable
CC of inducing cell death and can be used to develop products to mediate or
CC inhibit apoptosis. The methods can be used for reducing the severity of
CC a proapoptotic dependence domain mediated pathological conditions e.g.
CC Huntington's disease, Alzheimer's disease, Kennedy's disease,
CC Spinocerebellar ataxias, dentatorubropallidoluysian atrophy,
CC Machado-Joseph disease, stroke or head trauma. They can also be used for
CC reducing the severity of a pathological condition mediated by upregulated
CC cell proliferation or cell survival e.g. neoplastic, malignant,
CC autoimmune or fibrotic conditions. This sequence encodes a human
CC androgen receptor described in the method of the invention.
XX
SQ Sequence 3715 BP; 841 A; 1055 C; 1001 G; 818 T; 0 other;

Query Match 70.8%; Score 3595.8; DB 20; Length 3715;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3685; Conservative 0; Mismatches 7; Indels 45; Gaps 4;

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Qy   4026 gtgggccaaggccttgcctggcttccgcaacttacacgtggacgaccagatggctgtcat 4085
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Qy   4206 gtcccggatgtacagccagtgtgtccgaatgaggcacctctctcaagagtttggatggct 4265
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Qy   4266 ccaaatcacccccccaggaattcctgtgcatgaaagcactgctactcttcagcattattcc 4325
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Db   2919 ccaaatcacccccccaggaattcctgtgcatgaaagcactgctactcttcagcattattcc 2978

Qy   4326 agtggatgggctgaaaaatcaaaaattctttgatgaacttcgaatgaactacatcaagga 4385
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Db   2979 agtggatgggctgaaaaatcaaaaattctttgatgaacttcgaatgaactacatcaagga 3038

Qy   4386 actcgatcgtatcattgcatgcaaaagaaaaaatcccacatcctgctcaagacgcttcta 4445
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Qy   4446 ccagctcaccaagctcctggactccgtgcagcctattgcgagagagctgcatcagttcac 4505
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Qy   4506 ttttgacctgctaatcaagtcacacatggtgagcgtggactttccggaaatgatggcaga 4565
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Qy   4626 cacccagtgaagcattggaaaccctatttccccaccccagctcatgccccctttcagatg 4685
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Qy   4686 tcttctgcctgttataactctgcactactcctctgcagtgccttggggaatttcctctat 4745
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RESULT   2
AAQ12001
ID   AAQ12001 standard; cDNA; 3715 BP.
XX
AC   AAQ12001;
XX
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DT   20-AUG-1991  (first entry)
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DE   Full-length human androgen receptor coding sequence.
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KW   hAR; DNA-binding protein; steroid hormone; ss.
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OS   Homo sapiens.
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FH   Key             Location/Qualifiers
FT   CDS             532..3288
FT                   /*tag= a
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FT                   /note= "includes shorter 734 residue hAR"
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PN   WO9107423-A.
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PD   30-MAY-1991.
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PF   19-OCT-1990;   90WO-US06015.
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PR   17-NOV-1989;   89US-0438775.
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PA   (ARCH-) ARCH DEV CORP.
XX
PI   Liao S,  Chang C;
XX
DR   WPI; 1991-178048/24.
DR   P-PSDB; AAR12223.
XX
PT   Androgen receptor and TR2 DNA binding proteins - DNA sequences
PT   and antibodies for detection and quantification methods
XX
PS   Claim 4; Fig 3; 79pp; English.
XX
CC   This sequence was isolated by screening commercially available human
CC   testis and prostate lambda gt11 cDNA libraries. Initial screening
CC   was with probes designed for homology to nucleotide sequences in the
CC   DNA-binding domain of known steroid receptors. Positive clones were
CC   then screened with 24mer probes specific for the various steroid
CC   receptors to eliminate those which coded for known receptors. Any
CC   remaining clones were analysed by restriction mapping and were
CC   sequenced. The human AR coding sequence is given here.
XX
SQ   Sequence 3715 BP; 842 A; 1055 C; 1003 G; 815 T; 0 other;
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Query Match 70.7%; Score 3594.2; DB 12; Length 3715;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3684; Conservative 0; Mismatches 8; Indels 45; Gaps 4;

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Qy   1395 caccccgagtgcggagccagagatcaaaagatgaaaaggcagtcaggtcttcagtagcca 1454
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     64 caccccgagtgcggag-cagagatcaaaagatgaaaaggcagtcaggtcttcagtagcca 122

Qy   1455 aaaaacaaaacaaacaaaaacaaaaaagccgaaataaaagaaaaagataataactcagtt 1514
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Db    123 aaaaacaaaacaaacaaaaacaaaaaagccgaaataaaagaaaaagataataactcagtt 182

Qy   1515 cttatttgcacctacttcagtggacactgaatttggaaggtggaggattttgttttttttc 1574
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Qy   1575 ttttaagatctgggcatcttttgaatctacccttcaagtattaagagacagactgtgagc 1634
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Qy   1815 ggggaggcggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgca 1874
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Qy   1875 gttagggctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttcca 1934
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Qy   1935 gaatctgttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggc 1994
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1995 cgcgagcgcagcacctcccggcgccagtttgctgctgctgcagcagcagcagcagcagca 2054
          ||||||||||||||||||||||||||||||||||||||||||
Db    663 cgcgagcgcagcacctcccggcgccagtttgctgctgct---------------------- 701

Qy   2055 gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagac 2114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    702 ---gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagac 758

Qy   2115 tagccccaggcagcagcagcagcagggtgaggatggttctccccaagcccatcgtag 2174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2175 aggccccacaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggc 2234
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Qy   2475 atccgaaggcagcagcagcgggagagcgagggaggcctcgggggctcccacttcctccaa 2534
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Qy   2535 ggacaattacttaggggcacttcgaccatttctgacaacgccaaggagttgtgtaaggc 2594
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Qy   5046 ggaaatcaaaacaaaaa 5062
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Db   3688 ggaaatcaaaacaaaaa 3704


RESULT   3
AAT63407
ID   AAT63407 standard; cDNA; 3569 BP.
XX
AC   AAT63407;
XX
DT   22-JUN-1997  (first entry)
XX
DE   Androgen receptor cDNA.
XX
KW   Androgen receptor; acidic fibroblast growth factor; aFGF;
KW   antisense; benign prostatic hyperplasia; prostate cancer; therapy;
KW   ds.
XX
OS   Homo sapiens.
XX
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FT                   /*tag=  b
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FT                   /note= "antisense oligonucleotide preferred for
FT                         use in methods of the invention"
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FT                   /*tag=  d
FT                   /note= "antisense oligonucleotide preferred for
FT                         use in methods of the invention"
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PN   WO9711170-A1.
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PD   27-MAR-1997.
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PF   20-SEP-1996;   96WO-US15081.
XX
PR   20-SEP-1995;   95US-0004018.
XX
PA   (WORC-) WORCESTER FOUND BIOMEDICAL RES.
XX
PI   Zamecnik PA;
XX
DR   WPI; 1997-202879/18.
DR   P-PSDB; AAW14783.
XX
PT   Oligonucleotide(s) antisense to human androgen receptor and acidic
PT   FGF genes - used to inhibit gene expression, for the treatment of
PT   benign prostatic hyperplasia
XX
PS   Claim 2; Page 21-29; 51pp; English.
XX
CC   A cDNA clone (AAT63407) codes for the human androgen receptor
CC   (AAW14783).  Methods of selectively inhibiting the growth, or of
CC   killing, prostatic cells involve the use of antisense
CC   oligonucleotides (see also AAT63200, AAT63404-05) to this androgen
CC   receptor sequence or antisense oligonucleotides (see also AAT63406)
CC   to the human acidic fibroblast growth factor gene (see also
CC   AAT63197-99).  The methods are esp. useful for the treatment of
CC   benign prostatic hyperplasia and prostate cancer.
XX

SQ   Sequence 3569 BP; 796 A; 1009 C; 974 G; 790 T; 0 other;


  Query Match             69.8%;  Score 3547;  DB 18;  Length 3569;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3569;  Conservative    0;  Mismatches    0;  Indels   12;  Gaps    1;

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Db      1 taataactcagttcttatttgcacctacttcagtggacactgaatttggaaggtggagga 60

Qy   1562 ttttgttttttttcttttaagatctgggcatcttttgaatctacccttcaagtattaagag 1621
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Qy   1622 acagactgtgagcctagcagggcagatcttgtccaccgtgtgtcttcttctgcacgagac 1681
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Db    121 acagactgtgagcctagcagggcagatcttgtccaccgtgtgtcttcttctgcacgagac 180

Qy   1682 tttgaggctgtcagagcgctttttgcgtggttgctcccgcaagtttccttctctggagct 1741
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Qy   1742 tcccgcaggtgggcagctagctgcagcgactaccgcatcatcacagcctgttgaactctt 1801
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Qy   1802 ctgagcaagagaaggggaggcggggtaagggaagtaggtggaagattcagccaagctcaa 1861
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Qy   1862 ggatggaagtgcagttagggctgggaagggtctaccctcggccgccgtccaagacctacc 1921
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Qy   1922 gaggagctttccagaatctgttccagagcgtgcgcgaagtgatccagaacccgggcccca 1981
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Qy   1982 ggcacccagaggccgcgagcgcagcacctcccggcgccagtttgctgctgctgcagcagc 2041
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2042 agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2101
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Qy   2102 agcagcaagagactagccccaggcagcagcagcagcagcagggtgaggatggttctcccc 2161
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Qy   2222 agccgcagtcggccctggagtgccaccccgagagaggttgcgtcccagagcctggagccg 2281
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Qy   2402 ccgctgaccttaaagacatcctgagcgaggccagcaccatgcaactccttcagcaacagc 2461
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Qy   2462 agcaggaagcagtatccgaaggcagcagcagcgggagagcgagggaggcctcgggggctc 2521
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Qy   2582 agttgtgtaaggcagtgtcggtgtccatgggcctgggtgtggaggcgttggagcatctga 2641
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Qy   2642 gtccaggggaacagcttcgggggggattgcatgtacgccccacttttgggagttccacccg 2701
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Qy   2702 ctgtgcgtcccactccttgtgccccattggccgaatgcaaaggttctctgctagacgaca 2761
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Qy   3782 atctgaaactacaggaggaaggagaggcttccagcaccaccagccccactgaggagacaa 3841
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Qy   4142 atgtcaactccaggatgctctacttcgcccctgatctggttttcaatgagtaccgcatgc 4201
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RESULT 4
AAN91772
ID AAN91772 standard; cDNA; 3569 BP.
XX
AC AAN91772;
XX
DT 19-MAR-1990 (first entry)
XX
DE Human androgen receptor cDNA.
XX
KW Human androgen receptor; monoclonal antibody; ploYclonal antibody;
KW cancer; probe.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 363..3122
FT /*tag= a
XX
PN WO8909791-A.
XX
PD 19-OCT-1989.
XX
PF 13-APR-1989; 89WO-US01548.
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PR 14-APR-1988; 88US-0182646.
XX
PA (UYNC-) UNIVERSITY OF NORTH CAROLINA.
XX
PI French FS, Wilson EM, Joseph DR, Lubahn DB;
XX
DR WPI; 1989-324206/44.
DR P-PSDB; AAP93109.
XX
PT DNA encoding androgen receptor protein - useful for transforming
PT eukaryotic hosts for protein expression and subsequent antibody prodn.
XX
PS Disclosure; Fig. 4; 41pp; English.
XX
CC Complementary DNA sequences derived from the cDNA may be used as probes
CC detect the presence of androgen receptor (AR mRNA in tumour cells, and to
CC detect AR gene defects using DNA hybrisidation assays.
XX
SQ Sequence 3569 BP; 796 A; 1008 C; 975 G; 790 T; 0 other;

Query Match 69.8%; Score 3545.4; DB 10; Length 3569;
Best Local Similarity 99.6%; Pred. No. 0;
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Qy   1562 ttttgtttttttctttaagatctgggcatcttttgaatctacccttcaagtattaagag 1621
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Qy   1742 tcccgcaggtgggcagctagctgcagcgactaccgcatcatcacagcctgttgaactctt 1801
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RESULT 5
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ID AAN91773 standard; cDNA; 4180 BP.
XX
AC AAN91773;
XX
DT 19-MAR-1990 (first entry)
XX
DE Rat androgen receptor cDNA.
XX
KW Rat androgen receptor; monoclonal antibody; ploYclonal antibody;
KW cancer; probe.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 996..3702
FT /*tag= a
XX
PN WO8909791-A.
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PD 19-OCT-1989.
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PF 13-APR-1989; 89WO-US01548.
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PR 14-APR-1988; 88US-0182646.
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PA (UYNC-) UNIVERSITY OF NORTH CAROLINA.
XX
PI French FS, Wilson EM, Joseph DR, Lubahn DB;
XX
DR WPI; 1989-324206/44.
DR P-PSDB; AAP93110.
XX
PT DNA encoding androgen receptor protein - useful for transforming
PT eukaryotic hosts for protein expression and subsequent antibody prodn.
XX
PS Disclosure; Fig. 5; 41pp; English.
XX
CC Complementary DNA sequences derived from the cDNA may be used as probes
CC detect the presence of androgen receptor (AR) mRNA in tumour cells, and
CC to detect AR gene defects using DNA hybrisidation assays.
XX
SQ Sequence 4180 BP; 1024 A; 1149 C; 1083 G; 924 T; 0 other;

Query Match 48.9%; Score 2486.4; DB 10; Length 4180;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 3416; Conservative 0; Mismatches 664; Indels 306; Gaps 23;

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Qy   4542 ggactttccggaaatgatggcagagatcatctctgtgcaagtgcccaagatcctttctgg 4601

Db   3609 ggactttcctgaaatgatggcagagatcatctctgtgcaagtgcccaagatcctttctgg 3668

Qy   4602 gaaagtcaagcccatctatttccacacccagtgaagcattggaaaccctatttccccacc 4661

Db   3669 gaaagtcaagcccatctatttccacacacagtgaagatttggaaaccctaatacccaaac 3728

Qy   4662 ccagctcatgccccctttcagatgtcttctgcctgt--tataactctgcactactcctct 4719

Db   3729 ccaccttgt-tccctttcagatgtcttctgcctgttatataactctgcactacttctct 3787

Qy   4720 gcagtgcctt-ggggaatttcctctattgatgtacagtctgtcatgaacatgttcctgaa 4778

Db   3788 gcattgccttgggggaaattcctctactgatgtacagtctgtcatgaacatgttccccaa 3847

Qy   4779 ttctatttgctgggctttttttttctctttctctccttttcttttttcttcttccctccta 4838

Db   3848 ----------gttctatttcctgggcttttccttctttctttttttcttcttctctgcctc 3896

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Db   3897 ttttaccctcccatggcacattttgaatccgctgcgtgttgtggctcctgcctgtgtttt 3956

Qy   4899 gaatggtgttgtatgcctttaaatctgtgatgatcctcatatggcccagtgtcaagttgt 4958

Db   3957 gagttttgttgtatttcttcaagtctgtgatgatcttcttgtggcccagtgtcaa-ctgt 4015

Qy   4959 gcttgtttacagcac--tactctgtgccagccacacaaacgtttacttatcttatgccac 5016

Db   4016 gcttgtttatagcactgtgctgtgtgccaaccaagcaaatgtttactcaccttatgccat 4075

Qy   5017 gggaagtttagagagctaagattatctggggaaatcaaaacaaaaaacaagcaaacaaaa 5076

Db   4076 ggcaagtttagagagctataagtatcttgggaagaaacaaacagagagagtaaaaaaacc 4135

Qy   5077 aaaaaa 5082

Db   4136 aaaaaa 4141
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RESULT 6
AAQ12002
ID AAQ12002 standard; DNA; 3217 BP.
XX
AC AAQ12002;
XX
DT 20-AUG-1991 (first entry)
XX
DE Full-length rat androgen receptor coding sequence.
XX
KW rAR; DNA-binding protein; steroid hormone; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 33..2741
FT /*tag= a
FT /product= full-length (902 amino acids) rAR
FT /note= "includes 733 residue shorter rAR protein"
XX
PN WO9107423-A.
XX
PD 30-MAY-1991.
XX
PF 19-OCT-1990; 90WO-US06015.
XX
PR 17-NOV-1989; 89US-0438775.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Liao S, Chang C;
XX
DR WPI; 1991-178048/24.
DR P-PSDB; AAR12224.
XX
PT Androgen receptor and TR2 DNA binding proteins - DNA sequences
PT and antibodies for detection and quantification methods
XX
PS Claim 4; Fig 3; 79pp; English.
XX
CC This sequence was isolated by screening a rat ventral prostate
CC lambda gt11 library in E.coli Y1090. Initial screening
CC was with probes designed for homology to nucleotide sequences in the
CC DNA-binding domain of known steroid receptors. Positive clones were
CC then screened with 24mer probes specific for the various steroid
CC receptors to eliminate those which coded for known receptors. Any
CC remaining clones were analysed by restriction mapping and were
CC sequenced. The rat AR coding sequence is given here.
XX
SQ Sequence 3217 BP; 776 A; 873 C; 843 G; 725 T; 0 other;

Query Match 43.1%; Score 2189.2; DB 12; Length 3217;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 2726; Conservative 0; Mismatches 393; Indels 191; Gaps 11;

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Db      1 gaattcggtggaagctagagacaagctaaaggatggaggtgcagttagggctgggaaggg 60

Qy   1892 tctaccctcggccgccgtccaagacctaccgaggagctttccagaatctgttccagagcg 1951

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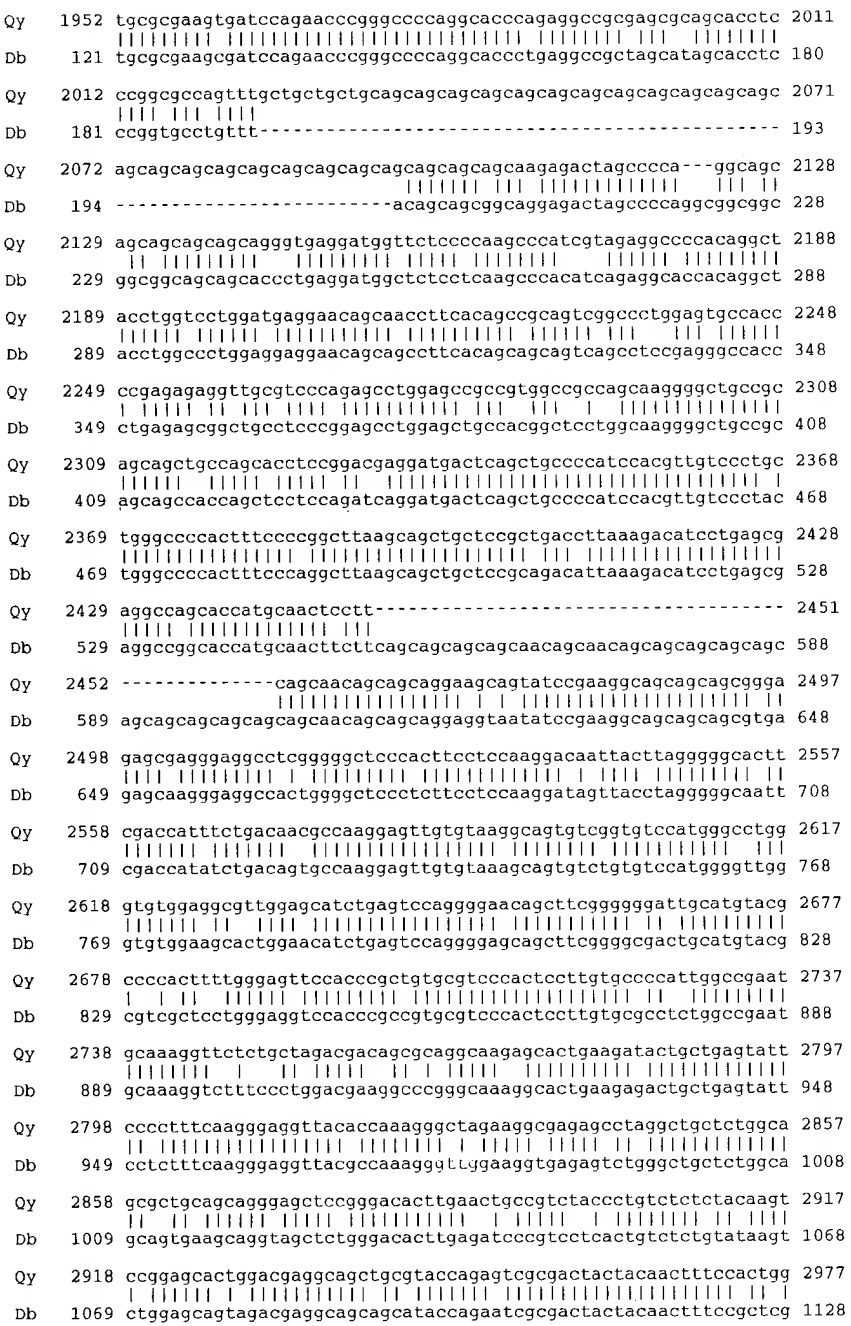

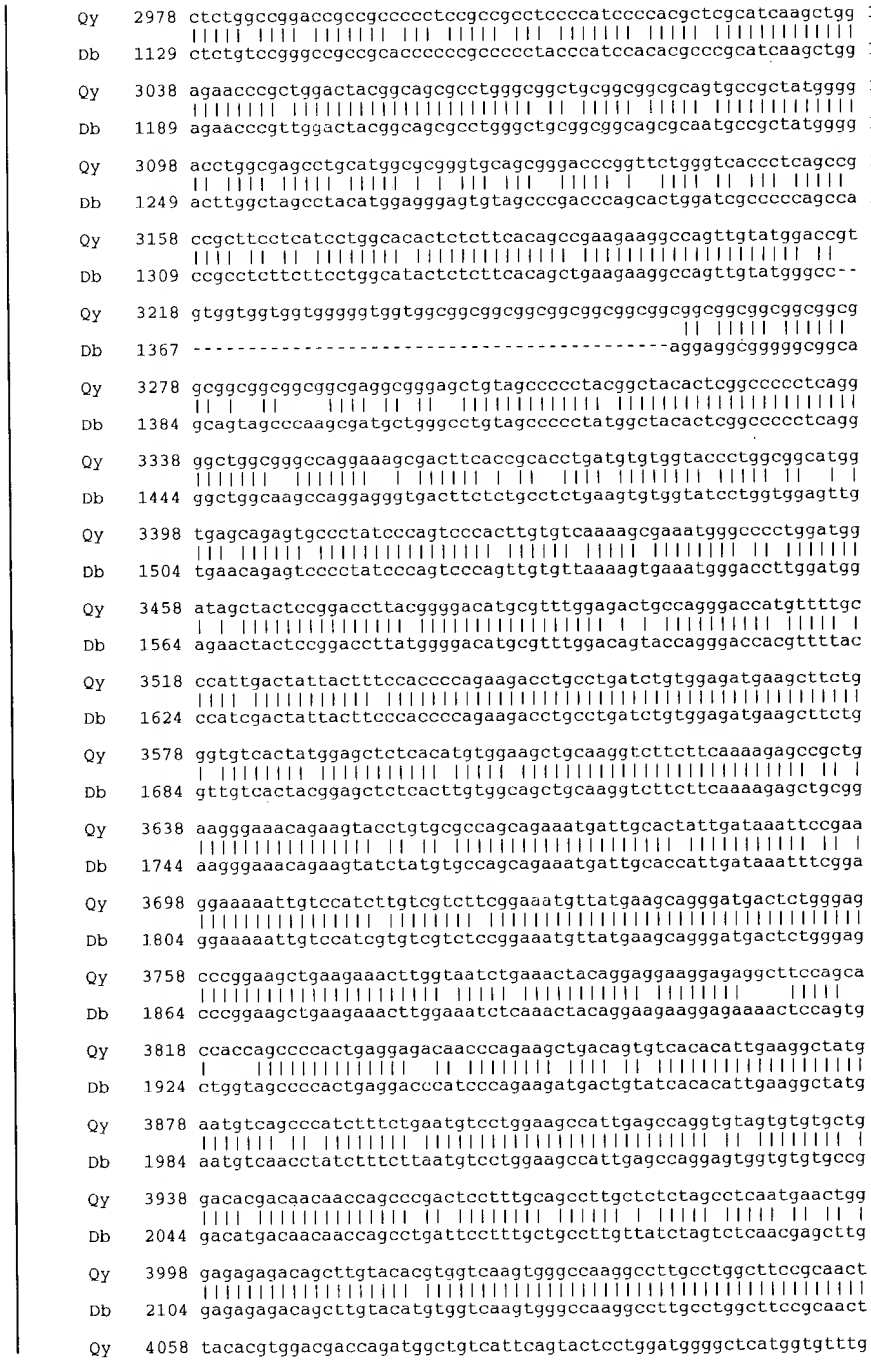

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Qy    4118 ccatgggctggcgatccttcaccaatgtcaactccaggatgctctacttcgcccctgatc 4177
Db    2224 ccatgggttggcggtccttcactaatgtcaactctaggatgctctactttgcacctgacc 2283

Qy    4178 tggttttcaatgagtaccgcatgcacaagtcccggatgtacagccagtgtgtccgaatga 4237
Db    2284 tggttttcaatgagtatcgcatgcacaagtctcgaatgtacagccagtgcgtgaggatga 2343

Qy    4238 ggcacctctctcaagagtttggatggctccaaatcacccccaggaattcctgtgcatga 4297
Db    2344 ggcacctttctcaagagtttggatggctccagataacccccaggaattcctgtgcatga 2403

Qy    4298 aagcactgctactcttcagcattattccagtggatgggctgaaaaatcaaaaattctttg 4357
Db    2404 aagcactgctactcttcagcattattccagtggatgggctgaaaaatcaaaaattctttg 2463

Qy    4358 atgaacttcgaatgaactacatcaaggaactcgatcgtatcattgcatgcaaaagaaaaa 4417
Db    2464 atgaacttcgaatgaactacatcaaggaacttgatcgcatcattgcatgcaaaagaaaaa 2523

Qy    4418 atcccacatcctgctcaagacgcttctaccagctcaccaagctcctggactccgtgcagc 4477
Db    2524 atcccacatcctgctcaaggcgcttctaccagctcaccaagctcctggattctgtgcagc 2583

Qy    4478 ctattgcgagagagctgcatcagttcacttttgacctgctaatcaagtcacacatggtga 4537
Db    2584 ctattgcaagagagctgcaacagttcacttttgacctgctaatcaagtcccatatggtga 2643

Qy    4538 gcgtggactttccggaaatgatggcagagatcatctctgtgcaagtgcccaagatccttt 4597
Db    2644 gcgtggactttcctgaaatgatggcagagatcatctctgtgcaagtgcccaagatccttt 2703

Qy    4598 ctgggaaagtcaagcccatctatttccacacccagtgaagcattggaaaccctatttccc 4657
Db    2704 ctgggaaagtcaagcccatctatttccacacacagtgaagatttggaaaccctaataccc 2763

Qy    4658 caccccagctcatgccccctttcagatgtcttctgcctgt--tataactctgcactactc 4715
Db    2764 aaacccaccttgt-tccctttcagatgtcttctgcctgttatataactctgcactactt 2822

Qy    4716 ctctgcagtgcctt-ggggaatttcctctattgatgtacagtctgtcatgaacatgttcc 4774
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Qy    4775 tgaattctatttgctgggctttttttttctctttctctcctttctttttcttcttccctc 4834
Db    2883 ccagttctatttcctgggctttt-----------ccttctttctttttcttcttctctg 2930

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Qy    4895 ttttgaatggtgttgtatgcctttaaatctgtgatgatcctcatatggcccagtgtcaag 4954
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Qy    4955 ttgtgcttgtttacagcac--tactctgtgccagccacacaaacgtttacttatcttatg 5012
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Qy    5013 ccacgggaagtttagagagctaagattatctggggaaatcaaaacaaaaaacaagcaaac 5072
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Qy    5073 aaaaaaaaaa 5082
Db    3169 aaccaaaaaa 3178

RESULT 7
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AAN91578
ID   AAN91578 standard; DNA; 3217 BP.
XX
AC   AAN91578;
XX
DT   28-FEB-1990  (first entry)
XX
DE   Rat androgen receptor DNA clone.
XX
KW   Androgen receptor; TR2 polypeptide;
XX
OS   Rat.
XX
FH   Key             Location/Qualifiers
FT   CDS             33..2739
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FT   CDS             541..2739
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PN   WO8909223-A.
XX
PD   05-OCT-1989.
XX
PF   24-MAR-1989;   89WO-US01238.
XX
PR   30-MAR-1988;   88US-0176107.
XX
PA   (ARCH-) ARCH DEVELOPMENT CORP.
XX
PI   Liao S,  Chang C;
XX
DR   WPI; 1989-309501/42.
DR   P-PSDB; AAP91006.
XX
PT   New DNA encoding new androgen receptor and TR2 polypeptide(s) - able
PT   to bind DNA, and derived antibodies, useful for receptor assay and
PT   purification.
XX
PS   Claim 8; fig. 3; 60pp; English.
XX
CC   The sequence is used to express the corresp. peptides and for
CC   hybridisation assays of RNA and DNA encoding androgen receptors.
CC   The 98 kD product starts at the first Met codon; the 79 kD product
CC   starts from the second.
XX
SQ   Sequence 3217 BP; 776 A; 874 C; 837 G; 730 T; 0 other;
```

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  Query Match           43.0%;  Score 2185.8;  DB 10;  Length 3217;
  Best Local Similarity  82.1%;  Pred. No. 0;
  Matches 2715;  Conservative    0;  Mismatches  407;  Indels  185;  Gaps   10;

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Qy    1892 tctaccctcggccgccgtccaagacctaccgaggagctttccagaatctgttccagagcg 1951
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Qy    1952 tgcgcgaagtgatccagaacccgggccccaggcaccccagaggccgcgagcgcagcacctc 2011
Db     121 tgcgcgaagcgatccagaacccgggccccaggcaccctgaggccgctagcatagcacctc 180

Qy    2012 ccggcgccagtttgctgctgctgcagcagcagcagcagcagcagcagcagcagcagc 2071
Db     181 ccggtgcctgttt---------------------------------------------- 193

Qy    2072 agcagcagcagcagcagcagcagcagcagcagcagaagagactagccccaggcagcagc 2131
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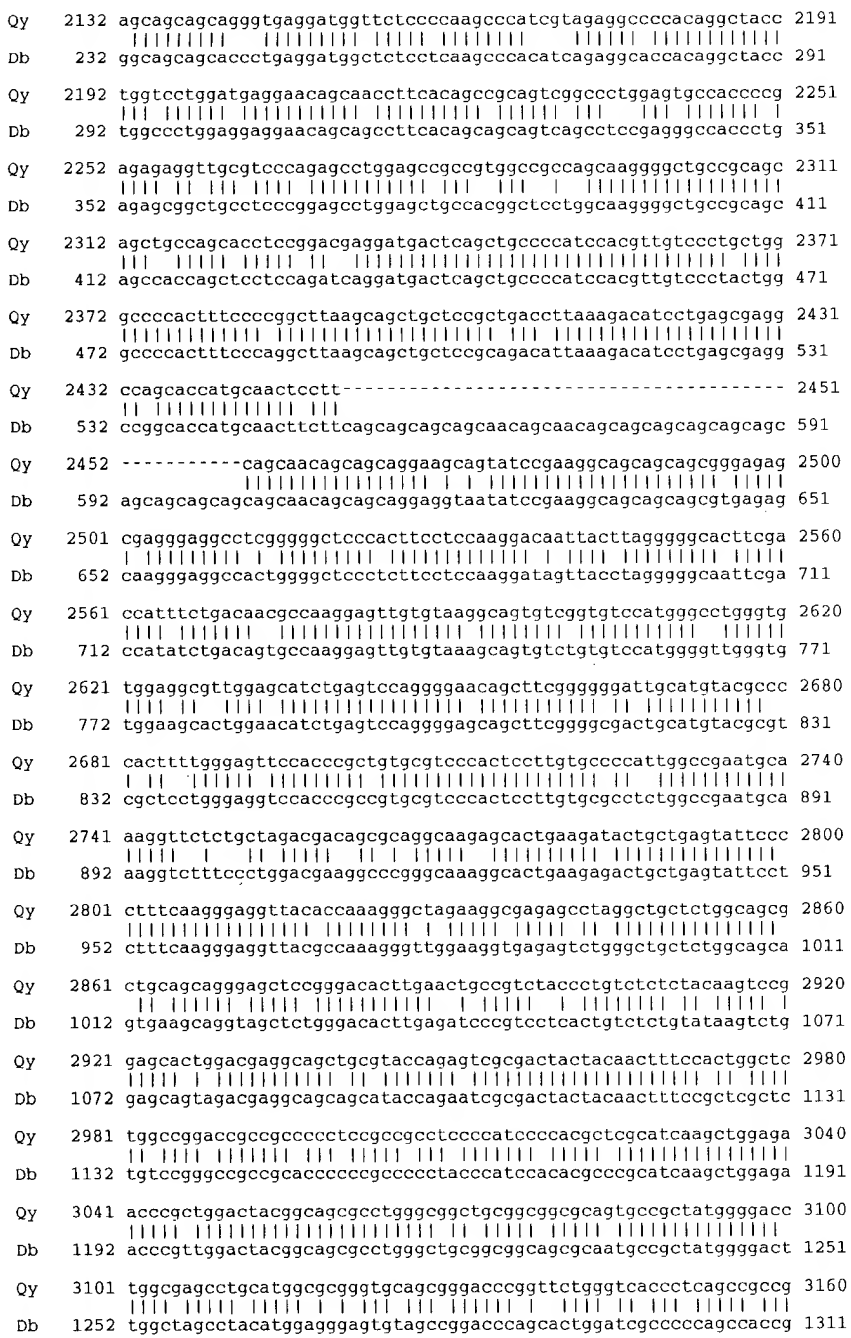
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Qy 2432 ccagcaccatgcaactcctt---------- 2451
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Qy    4601 ggaaagtcaagcccatctatttccacacccagtgaagcattggaaaccctatttccccac 4660
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Qy    4661 cccagctcatgccccctttcagatgtcttctgcctgt--tataactctgcactactcctc 4718
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Qy    4778 attctatttgctgggctttttttttctctttctctccttttcttttttcttcttccctccct 4837
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           |||||||||| ||||  | || ||||||| |||  |||| ||||||| | |||||||||
Db    3052 tgcttgtttatagcactgtgctgtgtgccaaccaagcaaatgtttactcaccttatgcca 3111

Qy    5016 cgggaagtttagagagctaagattatctggggaaatcaaaacaaaaaacaagcaaacaaa 5075
           || ||||||||||||||  | ||||| |||||   | ||  | | | |  ||| ||
Db    3112 tggcaagtttagagagctataagtatcttgggaagaaacaaacagagagagtaaaaaaac 3171

Qy    5076 aaaaaaa 5082
           |||||||
Db    3172 caaaaaa 3178


RESULT   8
AAF84342
ID   AAF84342 standard; DNA; 1810 BP.
XX
AC   AAF84342;
XX
DT   20-JUN-2001  (first entry)
XX
DE   Human androgen receptor gene.
XX
KW   Human; PCR primer; X chromosome inactivation; androgen receptor;
KW   methylation; HUMARA; ds.
XX
OS   Homo sapiens.
XX
PN   JP2001017199-A.
XX
PD   23-JAN-2001.
XX
PF   08-JUL-1999;   99JP-0194555.
XX
PR   08-JUL-1999;   99JP-0194555.
XX
PA   (MITP ) MITSUBISHI YUKA BCL KK.
XX
DR   WPI; 2001-285412/30.
XX
PT   Analysis of inactivated X chromosome useful for determining clonality
PT   and uniformity of growth of a cell population comprises analyzing
PT   methylation of human androgen receptor gene by a methyl-specific
PT   polymerase chain reaction -
XX
PS   Claim 2; Page 11-12; 14pp; Japanese.
XX
CC   The present invention relates to a method for analysis of inactivation of
CC   X chromosome. The method comprises analysing methylation of human
CC   androgen receptor (HUMARA) gene (the present sequence) by a
CC   methyl-specific polymerase chain reaction (PCR). The PCR primers amplify
CC   the base sequence of the region containing repeated number of
CC   polymorphism of CAG of the HUMARA gene, specific to methylation of the
CC   cytosine base at the 199th, the 203rd and the 206th or the 296th position
CC   of the present sequence. The method is useful for the detection of
CC   uniformity of cell growth, that is clonality.
XX
SQ   Sequence 1810 BP; 353 A; 565 C; 585 G; 307 T; 0 other;


  Query Match             33.8%;  Score 1715.6;  DB 22;  Length 1810;
  Best Local Similarity   98.7%;  Pred. No. 5.4e-285;
  Matches 1767;  Conservative    0;  Mismatches    4;  Indels   19;  Gaps    3;

Qy    1701 tttttgcgtggttgctcccgcaagtttccttctctggagcttcccgcaggtgggcagcta 1760
           |||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||
Db       1 tttttgcgtggttgctcccg-aagtttccttctctggagcttcccgcacgtgggcagcta 59

Qy    1761 gctgcagcgactaccgcatcatcacagcctgttgaactcttctgagcaagagaaggggag 1820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 gctgcagcgactaccgcatcatcacagcctgttgaactcttctgagcaagagaaggggag 119

Qy    1821 gcggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttagg 1880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 gcggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttagg 179

Qy    1881 gctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatct 1940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 gctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatct 239

Qy    1941 gttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgag 2000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 gttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgag 299

Qy    2001 cgcagcacctcccggcgccagtttgctgctgctgcagcagcagcagcagcagcagcagca 2060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 cgcagcacctcccggcgccagtttgctgctgct----------------gcagcagcagca 344

Qy    2061 gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagccc 2120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagccc 404

Qy    2121 caggcagcagcagcagcagcagggtgaggatggttctccccaagcccatcgtagaggccc 2180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 caggcagcagcagcagcagcagggtgaggatggttctccccaagcccatcgtagaggccc 464

Qy    2181 cacaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctgga 2240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 cacaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctgga 524
```

```
Qy   2241 gtgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaaggg 2300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 gtgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaaggg 584

Qy   2301 gctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgtt 2360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 gctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgtt 644

Qy   2361 gtccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacat 2420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 gtccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacat 704

Qy   2421 cctgagcgaggccagcaccatgcaactccttcagcaacagcagcaggaagcagtatccga 2480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 cctgagcgaggccagcaccatgcaactccttcagcaacagcagcaggaagcagtatccga 764

Qy   2481 aggcagcagcagcgggagagcgagggaggcctcgggggctcccacttcctccaaggacaa 2540
          |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    765 aggcagcagcagcgggagagcgagggagcgctcgggggctcccacttcctccaaggacaa 824

Qy   2541 ttacttaggggcacttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtc 2600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 ttacttaggggcacttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtc 884

Qy   2601 ggtgtccatgggcctgggtgtggaggcgttggagcatctgagtccaggggaacagcttcg 2660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 ggtgtccatgggcctgggtgtggaggcgttggagcatctgagtccaggggaacagcttcg 944

Qy   2661 gggggattgcatgtacgccccacttttgggagttccacccgctgtgcgtcccactccttg 2720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 gggggattgcatgtacgccccacttttgggagttccacccgctgtgcgtcccactccttg 1004

Qy   2721 tgccccattggccgaatgcaaaggttctctgctagacgacagccgcaggcaagagcactga 2780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 tgccccattggccgaatgcaaaggttctctgctagacgacagcgcaggcaagagcactga 1064

Qy   2781 agatactgctgagtattcccctttcaagggaggttacaccaaagggctagaaggcgagag 2840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 agatactgctgagtattcccctttcaagggaggttacaccaaagggctagaaggcgagag 1124

Qy   2841 cctaggctgctctggcagcgctgcagcagggagctccgggacacttgaactgccgtctac 2900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 cctaggctgctctggcagcgctgcagcagggagctccgggacacttgaactgccgtctac 1184

Qy   2901 cctgtctctctacaagtccggagcactggacgaggcagctgcgtaccagagtcgcgacta 2960
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Db   1185 cctgtctctctacaagtccggagcactggacgaggcagctgcgtaccagagtcgcgacta 1244

Qy   2961 ctacaactttccactggctctggccggaccgccgccccctccgccgcctccccatcccca 3020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1245 ctacaactttccactggctctggccggaccgccgccccctccgccgcctccccatcccca 1304

Qy   3021 cgctcgcatcaagctggagaacccgctggactacggcagcgcctgggcggctgcggcggc 3080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1305 cgctcgcatcaagctggagaacccgctggactacggcagcgcctgggcggctgcggcggc 1364

Qy   3081 gcagtgccgctatggggacctggcgagcctgcatggcgcgggtgcagcgggacccggttc 3140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1365 gcagtgccgctatggggacctggcgagcctgcatggcgcgggtgcagcgggacccggttc 1424

Qy   3141 tgggtcaccctcagccgccgcttcctcatcctggcacactctcttcacagccgaagaagg 3200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1425 tgggtcaccctcagccgccgcttcctcatcctggcacactctcttcacagccgaagaagg 1484

Qy   3201 ccagttgtatggaccgtgtggtggtggtgggggtggtggcggcggcggcggcggcggcgg 3260
          ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db   1485 ccagttgtatggaccgtgtggtggtggtgggggtggt---ggcggcggcggcggcggcgg 1541

Qy   3261 cggcggcggcggcggcggcggcggcggcgcggcgaggcgggagctgtagccccctacggcta 3320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1542 cggcggcggcggcggcggcggcggcggcggcgaggcgggagctgtagccccctacggcta 1601

Qy   3321 cactcggcccccctcaggggctggcgggccaggaaagcgacttcaccgcacctgatgtgtg 3380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1602 cactcggcccccctcaggggctggcgggccaggaaagcgacttcaccgcacctgatgtgtg 1661

Qy   3381 gtaccctggcggcatggtgagcagagtgccctatcccagtcccacttgtgtcaaaagcga 3440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1662 gtaccctggcggcatggtgagcagagtgccctatcccagtcccacttgtgtcaaaagcga 1721

Qy   3441 aatgggcccctggatggatagctactccggaccttacggggacatgcgtt 3490
          |||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1722 aatgggcccctggatggatagctactccggaccttacggggacatgcggt 1771
```

RESULT 9
AAQ12008
ID AAQ12008 standard; DNA; 1893 BP.
XX
AC AAQ12008;
XX
DT 20-AUG-1991 (first entry)
XX
DE TrpE/androgen receptor DNA-binding domain fusion gene.
XX
KW androgen receptor; AR; DNA-binding protein; steroid hormone; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	mat_peptide	1..969
FT		/*tag= a
FT		/product= 33kD trpE protein
FT		/note= "first 969bp of trpE coding region-
FT		multiple cloning region of pUC12"
FT	mat_peptide	1003..1839
FT		/*tag= bc
FT		/product= 29kD protein incl. AR DNA-binding domain

XX
PN WO9107423-A.
XX
PD 30-MAY-1991.
XX
PF 19-OCT-1990; 90WO-US06015.
XX
PR 17-NOV-1989; 89US-0438775.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Liao S, Chang C;
XX
DR WPI; 1991-178048/24.
DR P-PSDB; AAR12230.
XX
PT Androgen receptor and TR2 DNA binding proteins - DNA sequences
PT and antibodies for detection and quantification methods
XX
PS Example 13; Fig 10; 79pp; English.
XX
CC To express an androgen receptor fusion protein in E.coli, the pATH
CC expression system was used. The trpE is insoluble so partially
CC purified induced fusion protein is obtained by simply lysing the
CC E.coli and precipitating the insoluble fusion protein. The fusion
CC protein was used for immunisation to obtain monoclonal anti-AR
CC antibodies.
XX
SQ Sequence 1893 BP; 471 A; 474 C; 476 G; 472 T; 0 other;

Query Match 14.0%; Score 711.8; DB 12; Length 1893;
Best Local Similarity 90.3%; Pred. No. 3.7e-113;
Matches 761; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Qy   3555 gatctgtggagatgaagcttctgggtgtcactatggagctctcacatgtggaagctgcaa 3614
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```

```
Db   1002 gatctgtggagatgaagcttctggttgtcactacggagctctcacttgtggcagctgcaa 1061

Qy   3615 ggtcttcttcaaaagagccgctgaagggaaacagaagtacctgtgcgccagcagaaatga 3674
          |||||||||||||||||| || |||||||||||||||||| || || ||||||||||||||
Db   1062 ggtcttcttcaaaagagctgcggaagggaaacagaagtatctatgtgccagcagaaatga 1121

Qy   3675 ttgcactattgataaatttcgaaggaaaaattgtccatcttgtcgtcttcggaaatgtta 3734
          |||||| |||||||||| || |||||||||||||||||| |||||||| ||||||||||
Db   1122 ttgcaccattgataaatttcggaggaaaaattgtccatcgtgtcgtctccggaaatgtta 1181

Qy   3735 tgaagcagggatgactctgggagcccggaagctgaagaaacttggtaatctgaaactaca 3794
          |||||||||||||||||||||||| || |||||||||||||||| ||||| ||||||||
Db   1182 tgaagcagggatgactctgggagctcgtaagctgaagaaacttggaaatctcaaactaca 1241

Qy   3795 ggaggaaggagaggcttccagcaccaccagccccactgaggagacaacccagaagctgac 3854
          ||| ||||||||    ||||| |    |||||||||||||| || |||||||| ||||
Db   1242 ggaagaaggagaaaactccagtgctggtagccccactgaggacccatcccagaagatgac 1301

Qy   3855 agtgtcacacattgaaggctatgaatgtcagcccatctttctgaatgtcctggaagccat 3914
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Db   1302 tgtatcacacattgaaggctatgaatgtcaacctatctttcttaatgtcctggaagccat 1361

Qy   3915 tgagccaggtgtagtgtgtgctggacacgacaacaaccagcccgactcctttgcagcctt 3974
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Db   1362 tgagccaggagtggtgtgtgccggacatgacaacaaccagcctgattcctttgctgcctt 1421

Qy   3975 gctctctagcctcaatgaactgggagagagacagcttgtacacgtggtcaagtgggccaa 4034
          | | ||||| |||| || || || |||||||||||||||| ||||||||||||||||
Db   1422 gttatctagtctcaacgagcttggcgagagacagcttgtacatgtggtcaagtgggccaa 1481

Qy   4035 ggccttgcctggcttccgcaacttacacgtggacgaccagatggctgtcattcagtactc 4094
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Db   1482 ggccttgcctggcttccgcaacttgcatgtggatgaccagatggcagtcattcagtattc 1541

Qy   4095 ctggatggggctcatggtgtttgccatgggctggcgatccttcaccaatgtcaactccag 4154
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Qy   4155 gatgctctacttcgcccctgatctggttttcaatgagtaccgcatgcacaagtcccggat 4214
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Db   1602 gatgctctactttgcacctgacctggttttcaatgagtatcgcatgcacaagtctcgaat 1661

Qy   4215 gtacagccagtgtgtccgaatgaggcacctctctcaagagtttggatggctccaaatcac 4274
          |||||||||||| ||  | |||||||||||| |||||||||||||||||||||||| || ||
Db   1662 gtacagccagtgcgtgaggatgaggcacctttctcaagagtttggatggctccagataac 1721

Qy   4275 cccccaggaattcctgtgcatgaaagcactgctactcttcagcattattccagtggatgg 4334
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   1722 cccccaggaattcctgtgcatgaaagcagtgctactcttcagcattattccagtggatgg 1781

Qy   4335 gctgaaaaatcaaaaattctttgatgaacttcgaatgaactacatcaaggaactcgatcg 4394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1782 gctgaaaaatcaaaaattctttgatgaacttcgaatgaactacatcaaggaacttgatcc 1841

Qy   4395 tat 4397
          | |
Db   1842 tct 1844


RESULT  10
AAQ12007
ID   AAQ12007 standard; DNA; 1731 BP.
XX
AC   AAQ12007;
XX
DT   20-AUG-1991  (first entry)
XX
DE   TrpE/N-terminal domain of androgen receptor fusion gene.
XX
KW   androgen receptor; AR; DNA-binding protein; steroid hormone; ss.
XX
OS   Homo sapiens.
XX

FH   Key             Location/Qualifiers
FT   mat_peptide     1..969
FT                   /*tag=  a
FT                   /product= 33kD TrpE protein
FT                   /note= "first 969bp of trpE coding region-
FT                         multiple cloning region of pUC12"
FT   mat_peptide     988..1713
FT                   /*tag=  b
FT                   /product= 25kD N-terminal portion of AR
XX
PN   WO9107423-A.
XX
PD   30-MAY-1991.
XX
PF   19-OCT-1990;   90WO-US06015.
XX
PR   17-NOV-1989;   89US-0438775.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Liao S,  Chang C;
XX
DR   WPI; 1991-178048/24.
DR   P-PSDB; AAR12229.
XX
PT   Androgen receptor and TR2 DNA binding proteins - DNA sequences
PT   and antibodies for detection and quantification methods
XX
PS   Example 13; Fig 9; 79pp; English.
XX
CC   To express an androgen receptor fusion protein in E.coli, the pATH
CC   expression system was used. The trpE is insoluble so partially
CC   purified induced fusion protein is obtained by simply lysing the
CC   E.coli and precipitating the insoluble fusion protein. The fusion
CC   protein was used for immunisation to obtain monoclonal anti-AR
CC   antibodies.
XX
SQ   Sequence 1731 BP; 348 A; 510 C; 498 G; 375 T; 0 other;


  Query Match             13.8%;  Score 703.6;  DB 12;  Length 1731;
  Best Local Similarity   98.2%;  Pred. No. 9.3e-112;
  Matches  725;  Conservative    0;  Mismatches    4;  Indels    9;  Gaps    1;

Qy   2871 gagctccgggacacttgaactgccgtctaccctgtctctctacaagtccggagcactgga 2930
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Db    981 gagctcggggacacttgaactgccgtctaccctgtctctctacaagtccggagcactgga 1040

Qy   2931 cgaggcagctgcgtaccagagtcgcgactactacaactttccactggctctggccggacc 2990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041 cgaggcagctgcgtaccagagtcgcgactactacaactttccactggctctggccggacc 1100

Qy   2991 gccgccccctccgccgcctccccatccccacgctcgcatcaagctggagaacccgctgga 3050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 gccgccccctccgccgcctccccatccccacgctcgcatcaagctggagaacccgctgga 1160

Qy   3051 ctacggcagcgcctgggcggctgcggcggcgcagtgccgctatggggacctggcgagcct 3110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161 ctacggcagcgcctgggcggctgcggcggcgcagtgccgctatggggacctggcgagcct 1220

Qy   3111 gcatggcgcgggtgcagcgggacccggttctgggtcaccctcagccgccgcttcctcatc 3170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 gcatggcgcgggtgcagcgggacccggttctgggtcaccctcagccgccgcttcctcatc 1280

Qy   3171 ctggcacactctcttcacagccgaagaaggccagttgtatggaccgtgtggtggtggtgg 3230
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Db   1281 ctggcacactctcttcacagccgaagaaggccagttgtatggaccgtgtggtggtggtgg 1340

Qy   3231 gggtggt---------ggcggcggcggcggcggcggcggcggcggcggcggcggcggcgg 3281
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Db   1341 gggtggtggtggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcgg 1400

Qy   3282 cggcggcggcgaggcgggagctgtagccccctacggctacactcggcccccctcaggggct 3341
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          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 cggcggcggcgaggcggaagctgtagccccctacggctacactcggcccccctcaggggct 1460

Qy   3342 ggcgggccaggaaagcgacttcaccgcacctgatgtgtggtaccctggcggcatggtgag 3401
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461 ggcgggccaggaaagcgacttcaccgcacctgatgtgtggtaccctggcggcatggtgag 1520

Qy   3402 cagagtgccctatcccagtcccacttgtgtcaaaagcgaaatgggcccctggatggatag 3461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 cagagtgccctatcccagtcccacttgtgtcaaaagcgaaatgggcccctggatggatag 1580

Qy   3462 ctactccggaccttacggggacatgcgtttggagactgccagggaccatgttttgcccat 3521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 ctactccggaccttacggggacatgcgtttggagactgccagggaccatgttttgcccat 1640

Qy   3522 tgactattactttccaccccagaagacctgcctgatctgtggagatgaagcttctgggtg 3581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641 tgactattactttccaccccagaagacctgcctgatctgtggagatgaagcttctgggtg 1700

Qy   3582 tcactatggagctctcac 3599
          ||||||||||||||| | |
Db   1701 tcactatggagctcgccc 1718
```

RESULT 11
AAC70311
ID AAC70311 standard; DNA; 612 BP.
XX
AC AAC70311;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism containing sequence #47.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; ds.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US08440.
XX
PR 31-MAR-1999; 99US-0127248.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single
PT nucleotide polymorphisms, allele-specific oligonucleotides to the genes
PT are useful for phenotypic correlations, forensics, paternity testing,
PT medicine and genetic analysis -
XX
PS Claim 1; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases.
CC Note: The degenerate codon within the sequence represents the position
CC of an SNP, for example the letter S represents a polymorphism where the
CC nucleotide may be C or G.
XX
SQ Sequence 612 BP; 133 A; 178 C; 181 G; 119 T; 1 other;

```
  Query Match             12.0%;  Score 611.6;  DB 21;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-96;
  Matches  611;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2375 ccactttccccggcttaagcagctgctccgctgaccttaaagacatcctgagcgaggcca 2434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ccactttccccggcttaagcagctgctccgctgaccttaaagacatcctgagcgaggcca 60

Qy   2435 gcaccatgcaactccttcagcaacagcagcaggaagcagtatccgaaggcagcagcagcg 2494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gcaccatgcaactccttcagcaacagcagcaggaagcagtatccgaaggcagcagcagcg 120

Qy   2495 ggagagcgagggaggcctcgggggctcccacttcctccaaggacaattacttaggggca 2554
          |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggagagcgagggargcctcgggggctcccacttcctccaaggacaattacttaggggca 180

Qy   2555 cttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtcggtgtccatgggcc 2614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtcggtgtccatgggcc 240

Qy   2615 tgggtgtggaggcgttggagcatctgagtccaggggaacagcttcgggggattgcatgt 2674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tgggtgtggaggcgttggagcatctgagtccaggggaacagcttcgggggattgcatgt 300

Qy   2675 acgccccactttgggagttccacccgctgtgcgtcccactccttgtgccccattggccg 2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 acgccccactttgggagttccacccgctgtgcgtcccactccttgtgccccattggccg 360

Qy   2735 aatgcaaaggttctctgctagacgacagcgcaggcaagagcactgaagatactgctgagt 2794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aatgcaaaggttctctgctagacgacagcgcaggcaagagcactgaagatactgctgagt 420

Qy   2795 attcccctttcaagggaggttacaccaaagggctagaaggcgagagcctaggctgctctg 2854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 attcccctttcaagggaggttacaccaaagggctagaaggcgagagcctaggctgctctg 480

Qy   2855 gcagcgctgcagcagggagctccgggacacttgaactgccgtctaccctgtctctctaca 2914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gcagcgctgcagcagggagctccgggacacttgaactgccgtctaccctgtctctctaca 540

Qy   2915 agtccggagcactggacgaggcagctgcgtaccagagtcgcgactactacaactttccac 2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 agtccggagcactggacgaggcagctgcgtaccagagtcgcgactactacaactttccac 600

Qy   2975 tggctctggccg 2986
          ||||||||||||
Db    601 tggctctggccg 612
```

RESULT 12
AAC70335
ID AAC70335 standard; DNA; 612 BP.
XX
AC AAC70335;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism containing sequence #55.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; ds.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX

```
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US08440.
XX
PR   31-MAR-1999;   99US-0127248.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single
PT   nucleotide polymorphisms, allele-specific oligonucleotides to the genes
PT   are useful for phenotypic correlations, forensics, paternity testing,
PT   medicine and genetic analysis -
XX
PS   Claim 1; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases.
CC   Note: The degenerate codon within the sequence represents the position
CC   of an SNP, for example the letter S represents a polymorphism where the
CC   nucleotide may be C or G.
XX
SQ   Sequence 612 BP; 133 A; 178 C; 182 G; 118 T; 1 other;


  Query Match             12.0%;  Score 611.6;  DB 21;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 4.5e-96;
  Matches  611;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2375 ccactttccccggcttaagcagctgctccgctgaccttaaagacatcctgagcgaggcca 2434
           ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db      1 ccactttccccggcttaagcagctgcyccgctgaccttaaagacatcctgagcgaggcca 60

Qy   2435 gcaccatgcaactccttcagcaacagcagcaggaagcagtatccgaaggcagcagcagcg 2494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gcaccatgcaactccttcagcaacagcagcaggaagcagtatccgaaggcagcagcagcg 120

Qy   2495 ggagagcgagggaggcctcgggggctcccacttcctccaaggacaattacttaggggca 2554
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggagagcgagggaggcctcgggggctcccacttcctccaaggacaattacttaggggca 180

Qy   2555 cttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtcggtgtccatgggcc 2614
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cttcgaccatttctgacaacgccaaggagttgtgtaaggcagtgtcggtgtccatgggcc 240

Qy   2615 tgggtgtggaggcgttggagcatctgagtccaggggaacagcttcgggggattgcatgt 2674
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tgggtgtggaggcgttggagcatctgagtccaggggaacagcttcgggggattgcatgt 300

Qy   2675 acgccccacttttgggagttccacccgctgtgcgtcccactccttgtgccccattggccg 2734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 acgccccacttttgggagttccacccgctgtgcgtcccactccttgtgccccattggccg 360

Qy   2735 aatgcaaaggttctctgctagacgacagcgcaggcaagagcactgaagatactgctgagt 2794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aatgcaaaggttctctgctagacgacagcgcaggcaagagcactgaagatactgctgagt 420

Qy   2795 attcccctttcaagggaggttacaccaaagggctagaaggcgagagcctaggctgctctg 2854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 attcccctttcaagggaggttacaccaaagggctagaaggcgagagcctaggctgctctg 480

Qy   2855 gcagcgctgcagcagggagctccgggacacttgaactgccgtctaccctgtctctctaca 2914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 gcagcgctgcagcagggagctccgggacacttgaactgccgtctaccctgtctctctaca 540

Qy   2915 agtccggagcactggacgaggcagctgcgtaccagagtcgcgactactacaactttccac 2974
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 agtccggagcactggacgaggcagctgcgtaccagagtcgcgactactacaactttccac 600

Qy   2975 tggctctggccg 2986
           ||||||||||||
Db    601 tggctctggccg 612


RESULT  13
AAC70305
ID   AAC70305 standard; DNA; 598 BP.
XX
AC   AAC70305;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism containing sequence #45.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; ds.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US08440.
XX
PR   31-MAR-1999;   99US-0127248.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single
PT   nucleotide polymorphisms, allele-specific oligonucleotides to the genes
PT   are useful for phenotypic correlations, forensics, paternity testing,
PT   medicine and genetic analysis -
XX
PS   Claim 1; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases.
CC   Note: The degenerate codon within the sequence represents the position
CC   of an SNP, for example the letter S represents a polymorphism where the
CC   nucleotide may be C or G.
XX
SQ   Sequence 598 BP; 132 A; 197 C; 189 G; 79 T; 1 other;


  Query Match             11.3%;  Score 575.6;  DB 21;  Length 598;
  Best Local Similarity   97.9%;  Pred. No. 6.5e-90;
  Matches  597;  Conservative    1;  Mismatches    0;  Indels   12;  Gaps    1;

Qy   1822 cggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttaggg 1881
```

```
Db      1 cggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttaggg 60

Qy   1882 ctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatctg 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatctg 120

Qy   1942 ttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgagc 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgagc 180

Qy   2002 gcagcacctcccggcgccagtttgctgctgctgcagcagcagcagcagcagcagcagcag 2061
          ||||||||||||||||||||||||||||||||                ||||||||||||||||
Db    181 gcagcacctcccggcgccagtttgctgctgct------------gcagcagcagcagcag 228

Qy   2062 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagcccc 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagcccc 288

Qy   2122 aggcagcagcagcagcagcagggtgaggatggttctccccaagcccatcgtagaggcccc 2181
          ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db    289 aggcagcagcagcagcagcagggkgaggatggttctccccaagcccatcgtagaggcccc 348

Qy   2182 acaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctggag 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 acaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctggag 408

Qy   2242 tgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaagggg 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 tgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaagggg 468

Qy   2302 ctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgttg 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 ctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgttg 528

Qy   2362 tccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacatc 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 tccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacatc 588

Qy   2422 ctgagcgagg 2431
          ||||||||||
Db    589 ctgagcgagg 598
```

```
RESULT 14
AAC70308
ID   AAC70308 standard; DNA; 598 BP.
XX
AC   AAC70308;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism containing sequence #46.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; ds.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US08440.
XX
PR   31-MAR-1999;   99US-0127248.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single
PT   nucleotide polymorphisms, allele-specific oligonucleotides to the genes
PT   are useful for phenotypic correlations, forensics, paternity testing,
PT   medicine and genetic analysis -
XX
PS   Claim 1; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases.
CC   Note: The degenerate codon within the sequence represents the position
CC   of an SNP, for example the letter S represents a polymorphism where the
CC   nucleotide may be C or G.
XX
SQ   Sequence 598 BP; 132 A; 197 C; 188 G; 80 T; 1 other;
```

```
  Query Match             11.3%;  Score 575.6;  DB 21;  Length 598;
  Best Local Similarity   97.9%;  Pred. No. 6.5e-90;
  Matches  597;  Conservative    1;  Mismatches    0;  Indels   12;  Gaps    1;

Qy   1822 cggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttaggg 1881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 cggggtaagggaagtaggtggaagattcagccaagctcaaggatggaagtgcagttaggg 60

Qy   1882 ctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatctg 1941
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ctgggaagggtctaccctcggccgccgtccaagacctaccgaggagctttccagaatctg 120

Qy   1942 ttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgagc 2001
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ttccagagcgtgcgcgaagtgatccagaacccgggccccaggcacccagaggccgcgagc 180

Qy   2002 gcagcacctcccggcgccagtttgctgctgctgcagcagcagcagcagcagcagcagcag 2061
          ||||||||||||||||||||||||||||||||            ||||||||||||||||
Db    181 gcagcacctcccggcgccagtttgctgctgct------------gcagcagcagcagcag 228

Qy   2062 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagcccc 2121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcaagagactagcccc 288

Qy   2122 aggcagcagcagcagcagcagggtgaggatggttctccccaagcccatcgtagaggcccc 2181
          ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db    289 aggcagcagcagcagcagcagggtsaggatggttctccccaagcccatcgtagaggcccc 348

Qy   2182 acaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctggag 2241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    349 acaggctacctggtcctggatgaggaacagcaaccttcacagccgcagtcggccctggag 408

Qy   2242 tgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaagggg 2301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    409 tgccaccccgagagaggttgcgtcccagagcctggagccgccgtggccgccagcaagggg 468

Qy   2302 ctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgttg 2361
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    469 ctgccgcagcagctgccagcacctccggacgaggatgactcagctgccccatccacgttg 528

Qy   2362 tccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacatc 2421
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    529 tccctgctgggccccactttccccggcttaagcagctgctccgctgaccttaaagacatc 588

Qy   2422 ctgagcgagg 2431
          ||||||||||
Db    589 ctgagcgagg 598
```

RESULT 15
AAQ76269
ID AAQ76269 standard; DNA; 6244 BP.
XX
AC AAQ76269;
XX
DT 17-JUL-1995 (first entry)
XX
DE PhCMV*-1-controlled progesterone receptor.
XX
KW tTA; transactivator; tetracycline-controllable transactivator;
KW conditional inactivation; homologous recombination; gene expression;
KW gene regulation; gene therapy; tetracycline-resistance; tetR;
KW transgenic animal; PhCMV*-1; promoter; tetO; CMV;
KW progesterone receptor; ds.
XX
OS Human cytomegalovirus Towne.
XX
PN WO9429442-A.
XX
PD 22-DEC-1994.
XX
PF 14-JUN-1994; 94WO-US06734.
XX
PR 14-JUN-1993; 93US-0076327.
XX
PA (BADI) BASF AG.
XX
PI Bujard H, Gossen M, Salfeld JG, Voss JW;
XX
DR WPI; 1995-036472/05.
XX
PT Regulatory systems using tetracycline-controllable transactivator
PT (tTA) - useful for conditional inactivation or modulation of
PT gene expression in a host cell or animal
XX
PS Disclosure; Page 54-58; 103pp; English.
XX
CC The minimal promoter PhCMV*-1 is based on the human CMV
CC intermediate-early promoter (with enhancer region removed), fused
CC to a tetracycline operator, tetO. The promoter is used to
CC express tTA transactivator in host cells. In clone pUHD BGR3
CC (given in AAQ76269), cDNA for rabbit progesterone receptor is under
CC the control of PhCMV*-1.
XX
SQ Sequence 6244 BP; 1483 A; 1749 C; 1610 G; 1402 T; 0 other;

Query Match 7.9%; Score 401.6; DB 16; Length 6244;
Best Local Similarity 60.6%; Pred. No. 5.5e-60;
Matches 678; Conservative 0; Mismatches 434; Indels 6; Gaps 1;

```
Qy   3525 ctattactttccaccccagaagacctgcctgatctgtggagatgaagcttctgggtgtca 3584
          ||   | |  | ||| |||||||  ||  ||||||||||| |||||||| || || |||||
Db   2333 cttcgagtcactacctcagaagatttgtttgatctgtggggatgaagcatcaggctgtca 2392

Qy   3585 ctatggagctctcacatgtggaagctgcaaggtcttcttcaaaagagccgctgaagggaa 3644
           |||||  |  ||||| ||||| ||||| |||||||||||| ||||| ||    |||||| |
Db   2393 ttatggtgtcctcacctgtgggagctgtaaggtcttctttaaaagggcaatggaagggca 2452

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